

AMENDMENTS TO THE CLAIMS:

Amend the claims as follows:

1. (Currently Amended) An isolated nucleic acid molecule consisting of SEQ ID NO: 1, its complete complementary form, or RNA form thereof.
2. (Currently Amended) An isolated nucleic acid molecule consisting of SEQ ID NO: 2, its complete complementary form, or RNA form thereof.
3. (Currently Amended) An isolated nucleic acid molecule
 - (i) that specifically hybridizes to SEQ ID NOs: 1 or 2, or
 - (ii) that specifically hybridizes to the RNA form of said SEQ ID NOs: 1 or 2 wherein T is replaced by U, or
 - (iii) that specifically hybridizes to the complete complementary form of said SEQ ID NOs: 1 or 2, or
 - (iv) that specifically hybridizes to a S. aureus specific fragment of at least 20 contiguous nucleotides of SEQ ID NOs: 1 or 2, or
 - (v) that specifically hybridizes to a S. aureus specific fragment of at least 20 contiguous nucleotides of the RNA form of SEQ ID NOs: 1 or 2 wherein T is replaced by U, or

(vi) that specifically hybridizes to a S. aureus specific fragment of at least 20 contiguous nucleotides to the complete complementary form of said SEQ ID NOs: 1 or 2, or [[thereof]], or

(vii) that specifically hybridizes to a S. aureus specific homologue of SEQ ID NOs: 1 or 2, or

(viii) that specifically hybridizes to a S. aureus specific homologue of SEQ ID NOs: 1 or 2, or

(ix) that specifically hybridizes to a S. aureus specific homologue of the RNA form of said SEQ ID NOs: 1 or 2 wherein T is replaced by U, or

(x) that specifically hybridizes to the complete complementary form of a S. aureus specific homologue of SEQ ID NOs: 1 or 2, or

(xi) that specifically hybridizes to a S. aureus specific homologue of a S. aureus specific fragment of at least 20 contiguous nucleotides of SEQ ID NOs: 1 or 2, or

(xii) that specifically hybridizes to a S. aureus specific homologue of a S. aureus specific fragment of at least 20 contiguous nucleotides of the RNA form of SEQ ID NOs: 1 or 2 wherein T is replaced by U, or

(xiii) that specifically hybridizes to a S. aureus specific homologue of a S. aureus specific fragment of at least 20 contiguous nucleotides to the complete complementary form of said SEQ ID NOs: 1 or 2

~~any of their homologues, for the detection and/or identification of *Staphylococcus* species, in particular of *S. aureus*.~~

4. (Currently Amended) An isolated nucleic acid molecule according to claim 3 or claim 16, consisting of a nucleic acid selected from the group consisting of SEQ ID[[s]] NOs: 14, 16 to 23, 25 to 32, 35 to 42, 51, 52, 53, 55, 58, 65, 67, 68, 69 and 70.

5. (Currently Amended) A set of two polynucleotide probes, said two probes hybridizing specifically

to SEQ ID NO: 1 or

to SEQ ID NO: 2 or

to a *S. aureus* specific homologue of SEQ ID NO:1, or

to a *S. aureus* specific homologue of SEQ ID NO:2 homologues, or

to the RNA form of said SEQ ID NO: 1 wherein T is replaced by U, or

to the RNA form of said SEQ ID NO: 2 wherein T is replaced by U, or

to the RNA form of said *S. aureus* specific homologue of SEQ ID NO:1 wherein T is replaced by U, or

to the RNA form of said *S. aureus* specific homologue of SEQ ID NO:2 wherein T is replaced by U, or

to the complete complementary form of SEQ ID NO:1

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to the complete complementary form of SEQ ID NO:2

to the complete complementary form of the S. aureus specific homologue of SEQ ID NO:1, or

to the complete complementary form of the S. aureus specific homologue of SEQ ID NO:2, or

to the complete complementary form of the RNA form of said SEQ ID NO: 1 wherein T is replaced by U, or

to the complete complementary form of the RNA form of said SEQ ID NO: 2 wherein T is replaced by U, or

to the complete complementary form of the RNA form of said S. aureus specific homologue of SEQ ID NO:1 wherein T is replaced by U, or

to the complete complementary form of the RNA form of said S. aureus specific homologue of SEQ ID NO:2 wherein T is replaced by U,

~~their RNA form wherein T is replaced by U, or to~~

~~their complementary form, wherein said probes specifically hybridize to a S. aureus sequence within there are no more than 25 nucleotides of each other between said two probes.~~

6. (Currently Amended) A set of two polynucleotide probes according to claim 5 consisting of SEQ ID[[s]] NOs: 15 and 20, or SEQ ID[[s]] NOs: 15 and 21, or SEQ ID[[s]]

NOs: 17 and 16, or SEQ ID[[s]] NOs: 17 and 19, or SEQ ID[[s]] NOs: 26 and 14, or SEQ ID[[s]] NOs: 27 and 28, or SEQ ID[[s]] NOs: 29 and 22, or SEQ ID[[s]] NOs: 32 and 39, or SEQ ID[[s]] NOs: 32 and 23, or SEQ ID[[s]] NOs: 30 and 18, or SEQ ID[[s]] NOs: 36 and 38, or SEQ ID[[s]] NOs: 37 and 35, or SEQ ID[[s]] NOs: 40 and 25, or SEQ ID[[s]] NOs: 41 and 31, or SEQ ID[[s]] NOs: 42 and 43.

7. (Currently Amended) A composition comprising at least one nucleic acid molecule according to claim 1 and/or a set of two polynucleotide probes of claim 5
~~hybridizing specifically to SEQ ID NO 1 or SEQ ID NO 2 or homologues, or to their RNA form wherein T is replaced by U, or to their complementary form, wherein there are no more than 25 nucleotides between said two probes.~~

8. (Withdrawn – Currently Amended) A method for the detection and/or identification of ~~Staphylococcus~~ species, in particular *S. aureus*, comprising detecting the presence of a nucleic acid molecule of claim 3 in a composition suspected of containing *S. aureus* nucleic acid molecules, using a nucleic acid molecule as defined in claim 1 or 2 wherein in the RNA form T is replaced by U or a fragment of at least 20 contiguous nucleotides thereof, or any of their homologues.

9. (Withdrawn – Currently Amended) A method for detecting or identifying *S. aureus*, comprising detecting the presence of a nucleic acid molecule of claim 1 or claim 2 in a composition suspected of containing *S. aureus* nucleic acid molecules ~~Staphylococcus~~ species using at least one nucleic acid molecule according to claim 1.

10. (Withdrawn – Currently Amended) A method according to claim 9 for detection and/or identification of *Staphylococcus* species in a sample comprising the steps of:

- (i) optionally, if need be releasing, isolating and/or concentrating the polynucleic acids in the sample;
- (ii) optionally, if need be amplifying the 16S-23S rRNA spacer region, or a fragment comprising the target sequence, or the target sequence or a fragment thereof, with at least one suitable primer pair;
- (iii) hybridizing the polynucleic acids of step (i) or (ii) with at least one polynucleotide probe that hybridizes to the target sequence,
wherein the target sequence of step (ii) and (iii) consists of a nucleic acid molecule of

SEQ ID NO: 1 or

SEQ ID NO: 2 or

a *S. aureus* specific homologue of SEQ ID NO:1, or

a *S. aureus* specific homologue of SEQ ID NO:2, or

the RNA form of said SEQ ID NO: 1 wherein T is replaced by U, or

the RNA form of said SEQ ID NO: 2 wherein T is replaced by U, or

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the RNA form of said S. aureus specific homologue of SEQ ID NO:1 wherein T is replaced by U, or

the RNA form of said S. aureus specific homologue of SEQ ID NO:2 wherein T is replaced by U, or

the complete complementary form of SEQ ID NO:1

the complete complementary form of SEQ ID NO:2

the complete complementary form of the S. aureus specific homologue of SEQ ID NO:1, or

the complete complementary form of the S. aureus specific homologue of SEQ ID NO:2, or

the complete complementary form of the RNA form of said SEQ ID NO: 1 wherein T is replaced by U, or

the complete complementary form of the RNA form of said SEQ ID NO: 2 wherein T is replaced by U, or

the complete complementary form of the RNA form of said S. aureus specific homologue of SEQ ID NO:1 wherein T is replaced by U, or

the complete complementary form of the RNA form of said S. aureus specific homologue of SEQ ID NO:2 wherein T is replaced by U,

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a S. aureus specific fragment of at least 20 contiguous nucleotides of SEQ ID

NO: 1 or

a S. aureus specific fragment of at least 20 contiguous nucleotides of SEQ ID

NO: 2 or

a S. aureus specific fragment of at least 20 contiguous nucleotides of a S. aureus
specific homologue of SEQ ID NO:1, or

a S. aureus specific fragment of at least 20 contiguous nucleotides of a S. aureus
specific homologue of SEQ ID NO:2, or

a S. aureus specific fragment of at least 20 contiguous nucleotides of the RNA
form of said SEQ ID NO: 1 wherein T is replaced by U, or

a S. aureus specific fragment of at least 20 contiguous nucleotides of the RNA
form of said SEQ ID NO: 2 wherein T is replaced by U, or

a S. aureus specific fragment of at least 20 contiguous nucleotides of the RNA
form of said S. aureus specific homologue of SEQ ID NO:1 wherein T is replaced by U,
or

a S. aureus specific fragment of at least 20 contiguous nucleotides of the RNA
form of said S. aureus specific homologue of SEQ ID NO:2 wherein T is replaced by U,
or

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a S. aureus specific fragment of at least 20 contiguous nucleotides of the complete complementary form of SEQ ID NO:1

a S. aureus specific fragment of at least 20 contiguous nucleotides of the complete complementary form of SEQ ID NO:2

a S. aureus specific fragment of at least 20 contiguous nucleotides of the complete complementary form of the S. aureus specific homologue of SEQ ID NO:1, or

a S. aureus specific fragment of at least 20 contiguous nucleotides of the complete complementary form of the S. aureus specific homologue of SEQ ID NO:2, or

a S. aureus specific fragment of at least 20 contiguous nucleotides of the complete complementary form of the RNA form of said SEQ ID NO: 1 wherein T is replaced by U, or

a S. aureus specific fragment of at least 20 contiguous nucleotides of the complete complementary form of the RNA form of said SEQ ID NO: 2 wherein T is replaced by U, or

a S. aureus specific fragment of at least 20 contiguous nucleotides of the complete complementary form of the RNA form of said S. aureus specific homologue of SEQ ID NO:1 wherein T is replaced by U, or

a S. aureus specific fragment of at least 20 contiguous nucleotides of the complete complementary form of the RNA form of said S. aureus specific homologue of SEQ ID NO:2 wherein T is replaced by U,

~~SEQ ID NO 1 or 2 or homologues thereof, or to their RNA form wherein T is replaced by U, or to their complementary form, or a to a fragment of at least 20 contiguous nucleotides thereof,~~

(iv) detecting the hybrids formed as a result of (iii), and

(v) interpreting said detecting the signal(s) obtained and inferring the presence of S. aureus Staphylococcus species and/or identifying the Staphylococcus species in the sample from said interpreting.

11. (Withdrawn – Currently Amended) A method according to claim 10 wherein
[[a]]the suitable primer pair consists of any combination of a forward primer polynucleotide selected from the group consisting of SEQ ID NO: 45, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 56, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 66, SEQ ID NO: 67, SEQ ID NO: 68, a S. aureus specific homologue of SEQ ID NO: 45, , a S. aureus specific homologue of SEQ ID NO: 49, a S. aureus specific homologue of SEQ ID NO: 50, a S. aureus specific homologue of SEQ ID NO: 52, a S. aureus specific homologue of SEQ ID NO: 56, a S. aureus specific homologue of SEQ ID NO: 61, a S. aureus specific homologue of SEQ ID NO: 63, a S. aureus specific homologue of SEQ ID NO: 64, a S. aureus specific homologue of SEQ ID NO: 65, a S. aureus specific homologue of SEQ ID NO: 66, a S. aureus specific homologue of SEQ ID NO: 67, and a S. aureus specific homologue of SEQ ID NO: 68, and their homologues, and a reverse primer polynucleotide selected from the group consisting of SEQ ID NO: 46, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 54, SEQ ID NO: 55,

SEQ ID NO: 57, SEQ ID NO: 58, SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 62,
and their homologues, a S. aureus specific homologue of SEQ ID NO: 46, a S. aureus
specific homologue of SEQ ID NO: 47, a S. aureus specific homologue of SEQ ID NO:
48, a S. aureus specific homologue of SEQ ID NO: 51, a S. aureus specific homologue
of SEQ ID NO: 53, a S. aureus specific homologue of SEQ ID NO: 54, a S. aureus
specific homologue of SEQ ID NO: 55, a S. aureus specific homologue of SEQ ID NO:
57, a S. aureus specific homologue of SEQ ID NO: 58, a S. aureus specific homologue
of SEQ ID NO: 59, a S. aureus specific homologue of SEQ ID NO: 60, and a S. aureus
specific homologue of SEQ ID NO: 62.

12. (Withdrawn – Currently Amended) A method according to claim 10 wherein
step (iii) comprises hybridizing the polynucleic acids of step (i) or (ii) with two of said
polynucleotide probes that hybridizes to the target sequence~~two polynucleotide probes~~
are used.

13. (Withdrawn – Currently Amended) A method according to claim 12 wherein
the two polynucleotide probes hybridize to the target sequence within 25 nucleotides
each other~~adjacent to each other with less than 25 nucleotides in between.~~

14. (Withdrawn – Currently Amended) A method according to claim 13 wherein
the two polynucleotide probes consist of polynucleotides of SEQ ID[[s]] NOS: 15 and 20,
or 15 and 21, or 17 and 16, or 17 and 19, or 26 and 14, or 27 and 28, or 29 and 22, or

32 and 39, or 32 and 23, or 30 and 18, or 36 and 38, or 37 and 35, or 40 and 25, or 41 and 31, or 42 and 43.

15. (Currently Amended) A kit for detection and/or identification of *Staphylococcus* species comprising the following components:

[[[-]]] at least one nucleic acid molecule according to claim 1 and/or a set of two polynucleotide probes of claim 5, and hybridizing specifically to SEQ ID NO 1 or SEQ ID NO 2 or homologues, or to their RNA form wherein T is replaced by U, or to their complementary form, wherein there are no more than 25 nucleotides between said two probes.

[[[-]]] a hybridization buffer, or components necessary for producing said buffer.

16. (Currently Amended) An isolated nucleic acid molecule of at most 100 contiguous nucleotides that specifically hybridizes to a nucleic acid molecule of claim 3 SEQ ID NO 2, or to the RNA form of said SEQ ID NO 2 wherein T is replaced by U, or to the complementary form of said SEQ ID NO 2, or to a fragment of at least 20 contiguous nucleotides thereof, or to any of their homologues, for the detection and/or identification of *Staphylococcus* species, in particular of *S. aureus*.